#5

FIG. 1

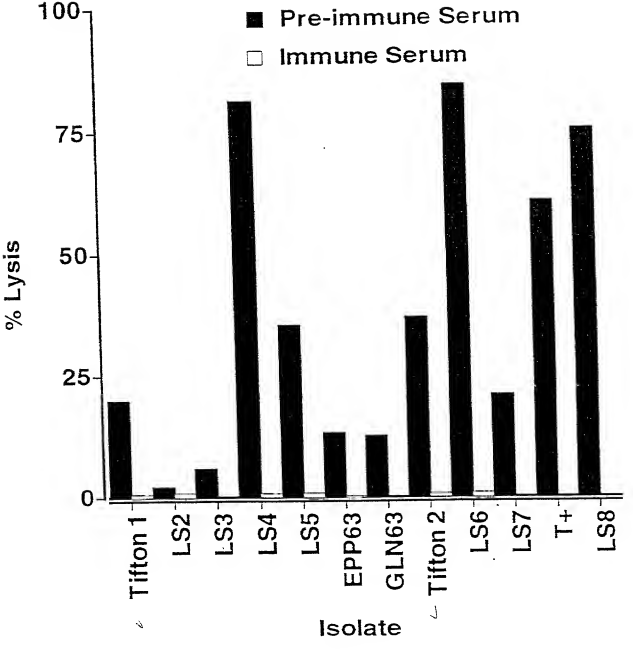

100
75
50
25
0
% Lysis
Pre-immune Serum
Immune Serum
Tifton 1
LS2
LS3
LS4
LS5
EPP63
GLN63
Tifton 2
LS6
LS7
T+
LS8
Isolate

FIG. 2

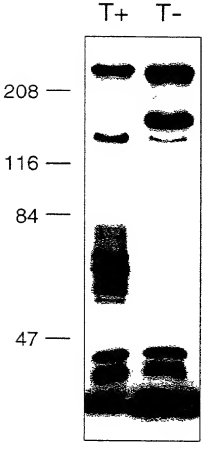


FIG 3-1

Appendix A update-July 1999

Bases 1-1200
Amino acids 1-400

```
   1 ATGTCCAATATAAATGTAATTAAATCTAATATTCAAGCAGGCTTGAATTCAACAAAGTCT   60
   1 M  S  N  I  N  V  I  K  S  N  I  Q  A  G  L  N  S  T  K  S    20

  61 GGATTAAAAAATCTTTACTTGGCTATTCCCAAAGATTATGATCCGCAAAAAGGTGGGACT  120
  21 G  L  K  N  L  Y  L  A  I  P  K  D  Y  D  P  Q  K  G  G  T    40

 121 TTAAATGATTTTATTAAAGCTGCTGATGAATTAGGTATTGCTCGTTTAGCAGAAGAGCCT  180
  41 L  N  D  F  I  K  A  A  D  E  L  G  I  A  R  L  A  E  E  P    60

 181 AATCACACTGAAACAGCAAAAAAATCTGTTGACACAGTAAATCAGTTTCTCTCTCTCACA  240
  61 N  H  T  E  T  A  K  K  S  V  D  T  V  N  Q  F  L  S  L  T    80

 241 CAAACTGGTATTGCTATTTCTGCAACAAAATTAGAAAAGTTCTTACAAAAACATTCTACC  300
  81 Q  T  G  I  A  I  S  A  T  K  L  E  K  F  L  Q  K  H  S  T   100

 301 AATAAGTTAGCCAAAGGGTTAGACAGTGTAGAAAATATTGATCGTAAATTAGGTAAAGCA  360
 101 N  K  L  A  K  G  L  D  S  V  E  N  I  D  R  K  L  G  K  A   120

 361 AGTAATGTATTATCAACATTAAGCTCTTTTTTGGGCACTGCATTAGCGGGTATAGAACTT  420
 121 S  N  V  L  S  T  L  S  S  F  L  G  T  A  L  A  G  I  E  L   140

 421 GATTCTTTAATCAAAAAAGGTGATGCTGCACCTGATGCTTTGGCTAAAGCTAGTATTGAC  480
 141 D  S  L  I  K  K  G  D  A  A  P  D  A  L  A  K  A  S  I  D   160

 481 TTGATTAATGAGATAATTGGTAATCTATCTCAGAGTACTCAAACGATTGAAGCATTTTCT  540
 161 L  I  N  E  I  I  G  N  L  S  Q  S  T  Q  T  I  E  A  F  S   180

 541 TCACAGTTAGCAAAGTTAGGTTCTACTATATCGCAGGCTAAAGGCTTCTCTAATATAGGA  600
 181 S  Q  L  A  K  L  G  S  T  I  S  Q  A  K  G  F  S  N  I  G   200

 601 AACAAGTTGCAAAACTTAAATTTTTCTAAAACAAATCTTGGTTTGGAAATAATTACTGGT  660
 201 N  K  L  Q  N  L  N  F  S  K  T  N  L  G  L  E  I  I  T  G   220

 661 TTGCTATCAGGCATTTCTGCAGGCTTTGCTTTAGCGGATAAAAATGCATCGACTGGCAAA  720
 221 L  L  S  G  I  S  A  G  F  A  L  A  D  K  N  A  S  T  G  K   240

 721 AAAGTTGCTGCAGGTTTTGAATTAAGCAATCAAGTTATTGGTAATGTAACAAAAGCAATT  780
 241 K  V  A  A  G  F  E  L  S  N  Q  V  I  G  N  V  T  K  A  I   260

 781 TCTTCATATGTTTTAGCACAACGTGTTGCTGCTGGTCTATCAACTACTGGTGCTGTTGCT  840
 261 S  S  Y  V  L  A  Q  R  V  A  A  G  L  S  T  T  G  A  V  A   280

 841 GCTTTAATTACTTCATCGATTATGTTGGCAATTAGTCCTTTGGCATTTATGAATGCAGCA  900
 281 A  L  I  T  S  S  I  M  L  A  I  S  P  L  A  F  M  N  A  A   300

 901 GATAAATTCAATCATGCTAATGCTCTTGATGAGTTTGCAAAACAATTCCGAAAATTTGGC  960
 301 D  K  F  N  H  A  N  A  L  D  E  F  A  K  Q  F  R  K  F  G   320

 961 TATGATGGGGATCATTTATTGGCTGAATATCAGCGTGGTGTGGGTACTATTGAAGCTTCA 1020
 321 Y  D  G  D  H  L  L  A  E  Y  Q  R  G  V  G  T  I  E  A  S   340

1021 TTAACTACAATTAGTACGGCATTAGGTGCAGTTTCTGCTGGTGTTTCCGCTGCTGCTGTA 1080
 341 L  T  T  I  S  T  A  L  G  A  V  S  A  G  V  S  A  A  A  V   360

1081 GGATCTGCTGTTGGTGCACCGATTGCACTATTAGTTGCAGGTGTTACAGGATTGATCTCT 1140
 361 G  S  A  V  G  A  P  I  A  L  L  V  A  G  V  T  G  L  I  S   380

1141 GGAATTTTAGAAGCGTCTAAACAGGCAATGTTTGAAAGTGTTGCTAACCGTTTACAAGGT 1200
 381 G  I  L  E  A  S  K  Q  A  M  F  E  S  V  A  N  R  L  Q  G   400
```

FIG 3-2

Appendix A update-July 1999, continued

Bases 1201-2400
Amino acids 401-800

```
1201 AAAATTTTAGAGTGGGAAAAGCAAAATGGCGGTCAGAACTATTTTGATAAAGGCTATGAT 1260
 401  K  I  L  E  W  E  K  Q  N  G  G  Q  N  Y  F  D  K  G  Y  D   420

1261 TCTCGTTATGCTGCTTATTTAGCTAATAACTTAAAATTTTTGTCTGAGCTAAATAAAGAG 1320
 421  S  R  Y  A  A  Y  L  A  N  N  L  K  F  L  S  E  L  N  K  E   440

1321 TTGGAAGCTGAACGTGTTATTGCAATCACCCAACAACGTTGGGATAATAATATTGGTGAG 1380
 441  L  E  A  E  R  V  I  A  I  T  Q  Q  R  W  D  N  N  I  G  E   460

1381 TTAGCAGGTATTACCAAATTGGGTGAACGCATTAAGAGCGGAAAAGCTTATGCAGATGCT 1440
 461  L  A  G  I  T  K  L  G  E  R  I  K  S  G  K  A  Y  A  D  A   480

1441 TTTGAAGATGGCAAGAAAGTTGAAGCTGGTTCCAATATTACTTTGGATGCTAAAACTGGT 1500
 481  F  E  D  G  K  K  V  E  A  G  S  N  I  T  L  D  A  K  T  G   500

1501 ATCATAGACATTAGTAATTCAAATGGGAAAAAAACGCAAGCGTTGCATTTCACTTCGCCT 1560
 501  I  I  D  I  S  N  S  N  G  K  K  T  Q  A  L  H  F  T  S  P   520

1561 TTGTTAACAGCAGGAACTGAATCACGTGAACGTTTAACTAATGGTAAATACTCTTATATT 1620
 521  L  L  T  A  G  T  E  S  R  E  R  L  T  N  G  K  Y  S  Y  I   540

1621 AATAAGTTAAAATTCGGACGTGTAAAAAACTGGCAAGTTACAGATGGAGAGGCTAGTTCT 1680
 541  N  K  L  K  F  G  R  V  K  N  W  Q  V  T  D  G  E  A  S  S   560

1681 AAATTAGATTTCTCTAAAGTTATTCAGCGTGTAGCCGAGACAGAAGGCACAGACGAGATT 1740
 561  K  L  D  F  S  K  V  I  Q  R  V  A  E  T  E  G  T  D  E  I   580

1741 GGTCTAATAGTAAATGCAAAAGCTGGCAATGACGATATCTTTGTTGGTCAAGGTAAAATG 1800
 581  G  L  I  V  N  A  K  A  G  N  D  D  I  F  V  G  Q  G  K  M   600

1801 AATATTGATGGTGGAGATGGACACGATCGTGTCTTCTATAGTAAAGACGGAGGATTTGGT 1860
 601  N  I  D  G  G  D  G  H  D  R  V  F  Y  S  K  D  G  G  F  G   620

1861 AATATTACTGTAGATGGTACGAGTGCAACAGAAGCAGGCAGTTATACAGTTAATCGTAAG 1920
 621  N  I  T  V  D  G  T  S  A  T  E  A  G  S  Y  T  V  N  R  K   640

1921 GTTGCTCGAGGTGATATCTACCATGAAGTTGTGAAGCGTCAAGAAACCAAGGTGGGTAAA 1980
 641  V  A  R  G  D  I  Y  H  E  V  V  K  R  Q  E  T  K  V  G  K   660

1981 CGTACTGAAACTATCCAGTATCGTGATTATGAATTAAGAAAAGTTGGGTATGGTTATCAG 2040
 661  R  T  E  T  I  Q  Y  R  D  Y  E  L  R  K  V  G  Y  G  Y  Q   680

2041 TCTACCGATAATTTGAAATCAGTAGAAGAAGTAATTGGTTCTCAATTTAATGATGTATTC 2100
 681  S  T  D  N  L  K  S  V  E  E  V  I  G  S  Q  F  N  D  V  F   700

2101 AAAGGTTCTAAATTCAACGACATATTCCATAGTGGTGAAGGTGATGATTTACTCGATGGT 2160
 701  K  G  S  K  F  N  D  I  F  H  S  G  E  G  D  D  L  L  D  G   720

2161 GGTGCTGGTGACGACCGCTTGTTTGGTGGTAAAGGCAACGATCGACTTTCTGGAGATGAA 2220
 721  G  A  G  D  D  R  L  F  G  G  K  G  N  D  R  L  S  G  D  E   740

2221 GGCGATGATTTACTCGATGGCGGTTCTGGTGATGATGTATTAAATGGTGGTGCTGGTAAT 2280
 741  G  D  D  L  L  D  G  G  S  G  D  D  V  L  N  G  G  A  G  N   760

2281 GATGTCTATATCTTTCGGAAAGGTGATGGTAATGATACTTTGTACGATGGCACGGGCAAT 2340
 761  D  V  Y  I  F  R  K  G  D  G  N  D  T  L  Y  D  G  T  G  N   780

2341 GATAAATTAGCATTTGCAGATGCAAATATATCTGATATTATGATTGAACGTACCAAAGAG 2400
 781  D  K  L  A  F  A  D  A  N  I  S  D  I  M  I  E  R  T  K  E   800
```

FIG 3-3

Appendix A update-July 1999, continued

Bases 2401-2784
Amino acids 801-927

```
2401 GGTATTATAGTTAAACGAAATGATCATTCAGGTAGTATTAACATACCAAGATGGTACATA   2460
 801  G  I  I  V  K  R  N  D  H  S  G  S  I  N  I  P  R  W  Y  I    820

2461 ACATCAAATTTACAAAATTATCAAAGTAATAAAACAGATCATAAAATTGAGCAACTAATT   2520
 821  T  S  N  L  Q  N  Y  Q  S  N  K  T  D  H  K  I  E  Q  L  I    840

2521 GGTAAAGATGGTAGTTATATCACTTCCGATCAAATTGATAAAATTTTGCAAGATAAGAAA   2580
 841  G  K  D  G  S  Y  I  T  S  D  Q  I  D  K  I  L  Q  D  K  K    860

2581 GATGGTACAGTAATTACATCTCAAGAATTGAAAAAGCTTGCTGATGAGAATAAGAGCCAA   2640
 861  D  G  T  V  I  T  S  Q  E  L  K  K  L  A  D  E  N  K  S  Q    880

2641 AAATTATCTGCTTCGGACATTGCAAGTAGCTTAAATAAGCTAGTTGGGTCAATGGCACTA   2700
 881  K  L  S  A  S  D  I  A  S  S  L  N  K  L  V  G  S  M  A  L    900

2701 TTTGGTACAGCAAATAGTGTGAGTTCTAACGCCTTACAGCCAATTACACAACCAACTCAA   2760
 901  F  G  T  A  N  S  V  S  S  N  A  L  Q  P  I  T  Q  P  T  Q    920

2761 GGAATTTTGGCTCCAAGTGTTTAG          SEQ ID NO: 1                2784
 921  G  I  L  A  P  S  V  *           SEQ ID NO: 2                 928
```

FIG. 4

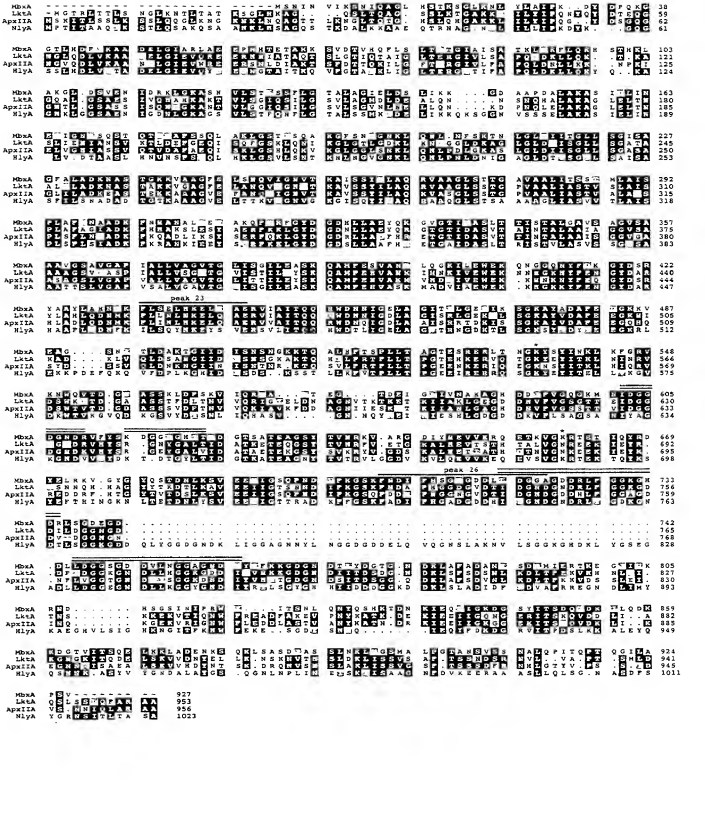


FIG.5

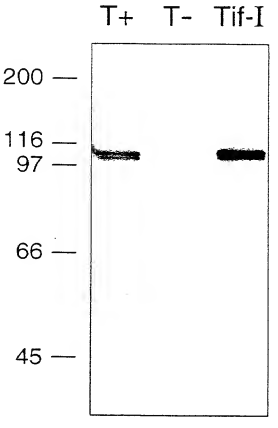

T+
T-
Tif-I
200
116
97
66
45

FIG.6

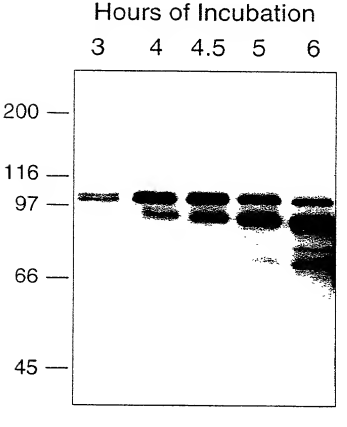
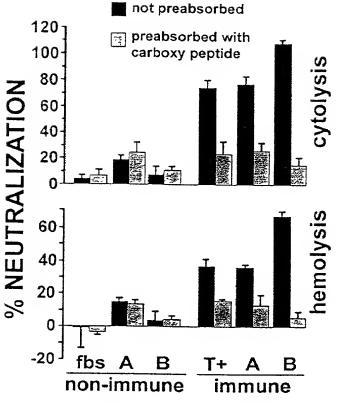

Hours of Incubation
3
4
4.5
5
6
200
116
97
66
45

FIG. 7


not preabsorbed
preabsorbed with carboxy peptide
% NEUTRALIZATION
120
100
80
60
40
20
0
cytolysis
60
40
20
0
-20
hemolysis
fbs A B
T+ A B
non-immune
immune

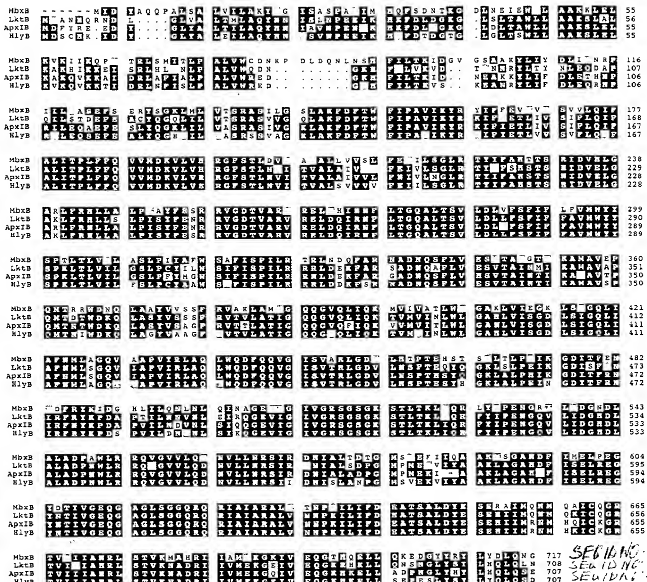
DNASIS Translation Editor [11-00 B gene.dna]

```
   1 ATGGGTGGTGATACTTCTTTAATTAGACTTAATTTACAAACCCTTAATAGTAATTTAGTT     60
   1  M  G  G  D  T  S  L  I  R     N  L  Q  T  L  N  S  N  L  V

  61 ATGATAGATTATGCTCAACAACCTGCTCTATCTGCTCTGGTTATCCTTGCCAAATACTAT    120
  21  M  I  D  Y  A  Q  Q  P  A  L  S  A  L  V  I  L  A  K  Y  Y     40

 121 GGTATTTCTGCAAGTCCAGCAGACATTATGCATCAGTTTTCTGATAATACAAAAGGAGAC    180
  41  G  I  S  A  S  P  A  D  I  M  H  Q  F  S  D  N  T  K  G  D     60

 181 CTGAATGAAATTGAATGGATGTTGGCAGCAAAGAAATTAGAATTAAAGGTAAAGATTATA    240
  61  L  N  E  I  E  W  M  L  A  A  K  K  L  E  L  K  V  K  I  I     80

 241 AAACAGCCTTTAACTCGATTGTCAATGATAACACTTCCTGCTTTGGTGTGGTGTGATAAT    300
  81  K  Q  P  L  T  R  L  S  M  I  T  L  P  A  L  V  W  C  D  N    100

 301 AAGCCCGATTTAGATCAAAATTTAAACTCTCATTTTATACTAACTAAAATTGATGGGGTG    360
 101  K  P  D  L  D  Q  N  L  N  S  H  F  I  L  T  K  I  D  G  V    120

 361 GGATCTGCTGCAAAATATCTCATCTACGATTTGATTGAGAATCGTCCCATAATATTAGAT    420
 121  G  S  A  A  K  Y  L  I  Y  D  L  I  E  N  R  P  I  I  L  D    140

 421 GCAAGTGAGTTTTCTGAAAGATATTCTGGTAAGTTAATGCTAGTAACTTCCCGTGCGTCA    480
 141  A  S  E  F  S  E  R  Y  S  G  K  L  M  L  V  T  S  R  A  S    160

 481 ATATTGGGTTCATTGGCTAAATTTGATTTTACTTGGTTTATTCCTGCGGTAATCAAATAT    540
 161  I  L  G  S  L  A  K  F  D  F  T  W  F  I  P  A  V  I  K  Y    180

 541 CGTTATATTTTTTTTGAAGTCATCGTTATTTCAGTGGTGCTACAGATTTTTGCTCTGATT    600
 181  R  Y  I  F  F  E  V  I  V  I  S  V  V  L  Q  I  F  A  L  I    200

 601 ACGCCATTGTTTTTTCAGGTTGTGATGGATAAGGTATTGGTGCATCGTGGTTTTTCTACT    660
 201  T  P  L  F  F  Q  V  V  M  D  K  V  L  V  H  R  G  F  S  T    220

 661 CTGGATGTGGTAGCGATTGCCTTGTTGGTAGTAAGTTTATTTGAAGTCATTTTAAGTGGT    720
 221  L  D  V  V  A  I  A  L  L  V  V  S  L  F  E  V  I  L  S  G    240

 721 CTACGCACTTATATTTTTGCTCATACAACCTCTCGAATTGATGTAGAGCTAGGAGCACGA    780
 241  L  R  T  Y  I  F  A  H  T  T  S  R  I  D  V  E  L  G  A  R    260

 781 TTATTTCGTCATCTATTAGCTCTACCGCTTGCTTATTTTGAGAGTAGAAGAGTAGGCGAT    840
 261  L  F  R  H  L  L  A  L  P  L  A  Y  F  E  S  R  R  V  G  D    280

 841 ACAGTTGCACGTATACGTGAATTGGAACATATCCGCAATTTCTTAACTGGTCAAGCTCTC    900
 281  T  V  A  R  I  R  E  L  E  H  I  R  N  F  L  T  G  Q  A  L    300

 901 ACTTCAGTTTTAGATTTGGTGTTTTCTTTTATATTCTTGTTTGTAATGTGGTATTACAGC    960
 301  T  S  V  L  D  L  V  F  S  F  I  F  L  F  V  M  W  Y  Y  S    320

 961 CCTACTTTAACACTGGTAGTTTTGGCATCATTACCAATATATGCGTTTTGGTCTGCCTTT   1020
 321  P  T  L  T  L  V  V  L  A  S  L  P  I  Y  A  F  W  S  A  F    340

1021 ATTAGCCCAATTTTACGCACTCGACTAAATGATCAATTTGCACGCAATGCAGATAATCAA   1080
 341  I  S  P  I  L  R  T  R  L  N  D  Q  F  A  R  N  A  D  N  Q   .360

1081 TCTTTTTTAGTGGAAAGTATTACTGCGGTTGGTACGGTAAAAGCAATGGCAGTTGAACCT   1140
 361  S  F  L  V  E  S  I  T  A  V  G  T  V  K  A  M  A  V  E  P    380

1141 CAAATGACCCGTCGCTGGGATAATCAATTAGCAGCTTATGTGGTTTCTAGTTTTCGGGTA   1200
 381  Q  M  T  R  R  W  D  N  Q  L  A  A  Y  V  V  S  S  F  R  V    400

1201 GCTAAGTTGGCAATGGTTGGGCAGCAAGGAGTACAACTCATTCAAAAGATGGTTATTGTG   1260
 401  A  K  L  A  M  V  G  Q  Q  G  V  Q  L  I  Q  K  M  V  I  V    420

1261 GCAACTCTATGGATTGGTGCAAAATTGGTAATTGAAGGCAAGCTATCGGTAGGTCAATTA   1320
 421  A  T  L  W  I  G  A  K  L  V  I  E  G  K  L  S  V  G  Q  L    440
```

```
1321 ATAGCATTTAATATGCTGGCAGGTCAGGTGGCCGCTCCTGTTATCCGCCTGGCACAGCTA   1380
 441  I  A  F  N  M  L  A  G  Q     A  A  P  V  I  R  L  A  Q  L   [illegible]

1381 TGGCAAGATTTTCAGCAAGTAGGTATTTCAGTGGCGAGATTGGGTGATATTTTAAATACT   1440
 461  W  Q  D  F  Q  Q  V  G  I  S  V  A  R  L  G  D  I  L  N  T    480

1441 CCAACTGAGCATTCTACATCTCGCTTAACTTTACCTGATATTAAGGGTGATATTACATTT   1500
 481  P  T  E  H  S  T  S  R  L  T  L  P  D  I  K  G  D  I  T  F    500

1501 GAAAATGTTGATTTTCGCTACAAAATAGATGGGCATTTAATATTACAGAATTTAAATTTA   1560
 501  E  N  V  D  F  R  Y  K  I  D  G  H  L  I  L  Q  N  L  N  L    520

1561 CAGATTAACGCTGGAGAGATACTAGGTATCGTAGGACGCTCTGGTTCAGGTAAATCAACA   1620
 521  Q  I  N  A  G  E  I  L  G  I  V  G  R  S  G  S  G  K  S  T    540

1621 TTGACAAAATTAGTACAGCGTTTATATGTACCAGAAAATGGGCGAATATTAGTTGATGGA   1680
 541  L  T  K  L  V  Q  R  L  Y  V  P  E  N  G  R  I  L  V  D  G    560

1681 AACGATTTGGCATTAGCTGATCCCGCTTGGCTGCGTCGCCAAGTGGGTGTTGTTTTGCAG   1740
 561  N  D  L  A  L  A  D  P  A  W  L  R  R  Q  V  G  V  V  L  Q    580

1741 GAAAATGTGTTACTCAATCGTAGTATTCGAGATAATATTGCCCTAACTGATACGGGCATG   1800
 581  E  N  V  L  L  N  R  S  I  R  D  N  I  A  L  T  D  T  G  M    600

1801 TCATTAGAGTTTATTATCCAGGCTGCCAAGATGTCTGGGGCACATGACTTTATTATGGAA   1860
 601  S  L  E  F  I  I  Q  A  A  K  M  S  G  A  H  D  F  I  M  E    620

1861 TTGCCTGAGGGTTATGATACGATTGTTGGAGAGCAAGGTGCAGGCTTGTCAGGTGGACAA   1920
 621  L  P  E  G  Y  D  T  I  V  G  E  Q  G  A  G  L  S  G  G  Q    640

1921 CGCCAGCGTATCGCTATTGCGCGTGCTTTAATTACCAATCCGCGTATTTTGATTTTTGAT   1980
 641  R  Q  R  I  A  I  A  R  A  L  I  T  N  P  R  I  L  I  F  D    660

1981 GAAGCTACTAGTGCATTAGACTATGAGTCGGAAAGGGCTATTATGCAAAATATGCAGGCA   2040
 661  E  A  T  S  A  L  D  Y  E  S  E  R  A  I  M  Q  N  M  Q  A    680

2041 ATTTGCCAAGGTAGAACAGTGTTGATTATTGCACATCGCTTATCTACCGTAAAAATGGCA   2100
 681  I  C  Q  G  R  T  V  L  I  I  A  H  R  L  S  T  V  K  M  A    700

2101 CATCGCATTATTGCAATGGACAAGGGGAAAATTGTAGAGCAAGGCACACATCAAGAATTG   2160
 701  H  R  I  I  A  M  D  K  G  K  I  V  E  Q  G  T  H  Q  E  L    720

2161 TTGCAAAAAGAAGATGGTTACTATCGTTATTTATATGATTTGCAGAATGGATAAA        2215
 721  L  Q  K  E  D  G  Y  Y  R  Y  L  Y  D  L  Q  N  G  *           739
```

FIG. 8-2

FIG.9



SEQ ID NO: 18
SEQ ID NO: 19
SEQ ID NO: 20
SEQ ID NO: 21

FIG. 10

```
DNASIS  Translation Editor [11-00 C gene.dna]
       1 ATGACGAAAAAGTTTGCAGAGCTAGGTTTAATTGCATGGCTTTGGTCTAACTCTGATATG     60
         1  M  T  K  K  F  A  E  L  G  L  I  A  W  L  W  S  N  S  D  M     20

      61 CATAAACATTGGACGTTGTCTTTGTTTGCGACCAATGTTATTCCGGCAATTGAGACAGGT    120
        21  H  K  H  W  T  L  S  L  F  A  T  N  V  I  P  A  I  E  T  G     40

     121 CAATATGTTATATTGAAAAGAGAAGATATGCCTGTAGCATATTGTAGTTGGGCTAAACTT    180
        41  Q  Y  V  I  L  K  R  E  D  M  P  V  A  Y  C  S  W  A  K  L     60

     181 AGTTTAGAAAACGAGGTTAAATATATTAACGATGTTACTTCTCTTAAGTTAGATGACTGG    240
        61  S  L  E  N  E  V  K  Y  I  N  D  V  T  S  L  K  L  D  D  W     80

     241 CAGTCAGGTGACCGAAACTGGTTTATTGACTGGATTGCTCCATTTGGCGATAGTCTTACA    300
        81  Q  S  G  D  R  N  W  F  I  D  W  I  A  P  F  G  D  S  L  T    100

     301 CTCACAAAACACATGAGAACGTTATTTTCAGATGAATTGTTTAGAGCGATTCGTGTAGAT    360
       101  L  T  K  H  M  R  T  L  F  S  D  E  L  F  R  A  I  R  V  D    120

     361 GGAAATTCATCGCATGGTAAGATATCTGAATTTTATGGAAAGTCTGTTGATTCAAAATTA    420
       121  G  N  S  S  H  G  K  I  S  E  F  Y  G  K  S  V  D  S  K  L    140

     421 GCCTCAAGAATATTTGCACAATATCACGAAGATTTGACGAGCAAATTGTCAACTCAGAAT    480
       141  A  S  R  I  F  A  Q  Y  H  E  D  L  T  S  K  L  S  T  Q  N    160

     481 AATTTTATTATATCTAAAGATAATTAA                                     507
       161  N  F  I  I  S  K  D  N  *                                    169
```

FIG. 11

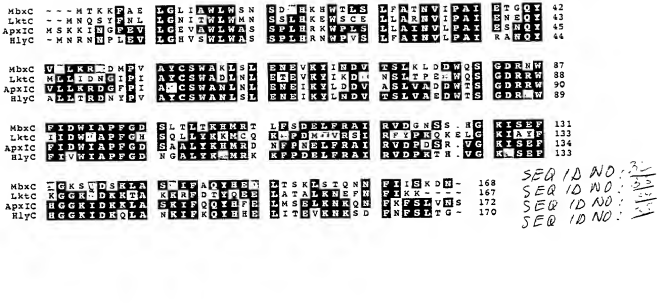


FIG 12-1

```
   1 ATGTTTATACAAGCACTTAAAGATTTTTTTATTCGCTATATAACCGTTTGGCGCAATACA     60
   1  M  F  I  Q  A  L  K  D  F     I  R  Y  I  T  V  W  R  N  T

  61 TGGGCAGTTCGAGACCAACTAACCCCTCCTAAGCGTACTAAAGAAGAACTCGCTTTTCTT    120
  21  W  A  V  R  D  Q  L  T  P  P  K  R  T  K  E  E  L  A  F  L     40

 121 CCTGCACATCTAGAACTCACTGACACACCTGTATCCAGATCTTCTAAGTGGACAGCTAGA    180
  41  P  A  H  L  E  L  T  D  T  P  V  S  R  S  S  K  W  T  A  R     60

 181 ATAATCATGATATTTGTCCTATTTGCTTTGCTATGGTCTTGGGTTGGACAGATTGACATT    240
  61  I  I  M  I  F  V  L  F  A  L  L  W  S  W  V  G  Q  I  D  I     80

 241 GTTGCTACAGCTTCAGGTAAAATTTCTTCAGGTAGCCGTAGCAAGACTATTCAATCTTTG    300
  81  V  A  T  A  S  G  K  I  S  S  G  S  R  S  K  T  I  Q  S  L    100

 301 GAAACAGCGATAGTTAAAGCAGTTTATGTACGTGATGGTCAAAATGTTCAACAAGGTGAA    360
 101  E  T  A  I  V  K  A  V  Y  V  R  D  G  Q  N  V  Q  Q  G  E    120

 361 ATATTAGTAGATTTAGTGGGAATCGGTTCAGATAGTGATGTTGCTCAGTCCGAGAAAGCC    420
 121  I  L  V  D  L  V  G  I  G  S  D  S  D  V  A  Q  S  E  K  A    140

 421 CTTCGAGCAGCGCAATTATCTAAGCTACGCCTTGAAGCAATTTTATCAGCATTAAATCAC    480
 141  L  R  A  A  Q  L  S  K  L  R  L  E  A  I  L  S  A  L  N  H    160

 481 CGTATTAATCCTCAGATTGATGTAGCATATGCAAAGTCTTTAAATATTTCAGAATCGGAA    540
 161  R  I  N  P  Q  I  D  V  A  Y  A  K  S  L  N  I  S  E  S  E    180

 541 ATTAATGAAGCTCAAACTTTAGCCCAAAATCAATATCAAGCATGGTTAGCACAAGATGAA    600
 181  I  N  E  A  Q  T  L  A  Q  N  Q  Y  Q  A  W  L  A  Q  D  E    200

 601 CAACTAAAATTAACCTTAAAAGGACATCAAGCAGAATTACAATCTGCTCGATCCCAAGAA    660
 201  Q  L  K  L  T  L  K  G  H  Q  A  E  L  Q  S  A  R  S  Q  E    220

 661 CAAAAGTTGGTTTCAGTTGGTGCAATTGAACATCAAAAGACTGATGATTATCGGAGTCTC    720
 221  Q  K  L  V  S  V  G  A  I  E  H  Q  K  T  D  D  Y  R  S  L    240

 721 AAAGCAGAAAATTTTATATCTGAGCATGCTTATCTAGAACAAGAAAGCAAATTACTTAGC    780
 241  K  A  E  N  F  I  S  E  H  A  Y  L  E  Q  E  S  K  L  L  S    260

 781 AATCAAAATGATTTACAAAGTACACGTAGTCAGATTCAAAAAATACAGGCTGCAATCATG    840
 261  N  Q  N  D  L  Q  S  T  R  S  Q  I  Q  K  I  Q  A  A  I  M    280

 841 CAAGCTGAACAGAACCGTATGTTATATACTCAAAATCTAAAACGTGATACATTAGAATCT    900
 281  Q  A  E  Q  N  R  M  L  Y  T  Q  N  L  K  R  D  T  L  E  S    300

 901 TTACGCCAAACCAATGAACAGATTAATCAATATACTGGTCAAACTAATAAAGCTAAGCAG    960
 301  L  R  Q  T  N  E  Q  I  N  Q  Y  T  G  Q  T  N  K  A  K  Q    320

 961 CGACAGAAATTGCTGAGTATTAAATCACCTGTTAATGGTACTATACAAGAGCTAACAGCT   1020
 321  R  Q  K  L  L  S  I  K  S  P  V  N  G  T  I  Q  E  L  T  A    340

1021 TATACTTTAGGTGGAGTTGTACAAGCAGCACAAAAAATTATGGTTGTGGCACCTAACGAT   1080
 341  Y  T  L  G  G  V  V  Q  A  A  Q  K  I  M  V  V  A  P  N  D  . 360

1081 AATCAAGTGGAAGTAGAGGTATTAGTGCTAAATAAAGATATCGGCTTTGTAAAAGCTGGG   1140
 361  N  Q  V  E  V  E  V  L  V  L  N  K  D  I  G  F  V  K  A  G    380

1141 CAGAATGTTATCATCAAAATCGAGAGTTTTCCTTATACACGTTATGGTTATTTAACAGGT   1200
 381  Q  N  V  I  I  K  I  E  S  F  P  Y  T  R  Y  G  Y  L  T  G    400

1201 AAAATAAAAAGTATTAGTCATGATGCTATAGAACATCAACATTTAGGTCTAGTGTATACT   1260
 401  K  I  K  S  I  S  H  D  A  I  E  H  Q  H  L  G  L  V  Y  T    420

1261 GCACTTGTTTCTCTTGATAAAAGCACATTAAATATAGATGGAGTAACAATCAACTTAACG   1320
 421  A  L  V  S  L  D  K  S  T  L  N  I  D  G  V  T  I  N  L  T    440
```

DNASIS Translation Editor [11-60 B gene.dna]

```
1321 CCAGGAATGAATGTTACTGCTGAAATTAAAACAGGTAAACGTCGTGTTTTGGATTATATA   1380
 441  P  G  M  N  V  T  A  E  I     T  G  K  R  R  V  L  D  Y  I

1381 TTAAGTCCATTGCAGACAAAAGTTGATGAAAGTTTTCGAGAACGCTAA               1428
 461  L  S  P  L  Q  T  K  V  D  E  S  F  R  E  R  *                476
```

FIG. 12-2

FIG. 13

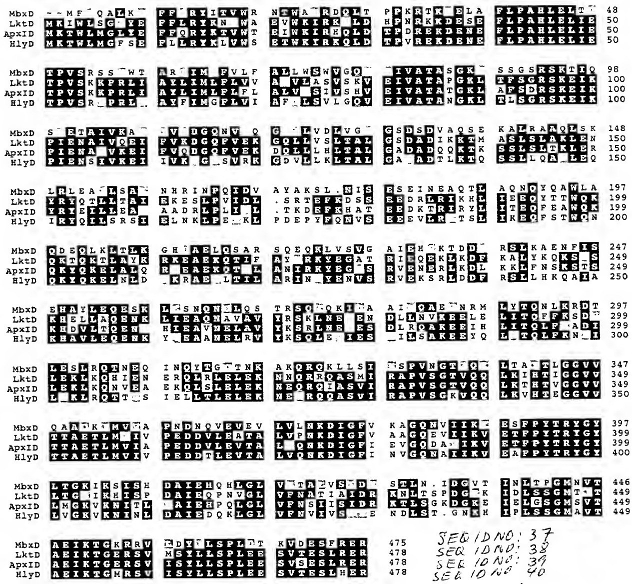
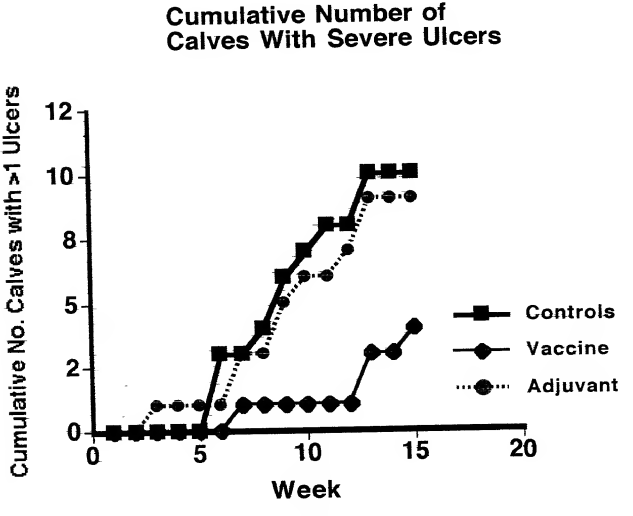

MbxD
LktD
ApxID
HlyD
SEQ ID NO: 37
SEQ ID NO: 38
SEQ ID NO: 39
SEQ ID NO: 40

FIG. 14



Number of calves with ulcers with clinical scores >+2

F1615

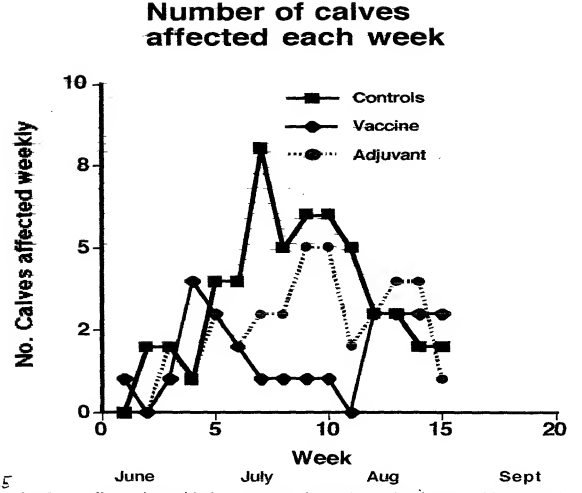
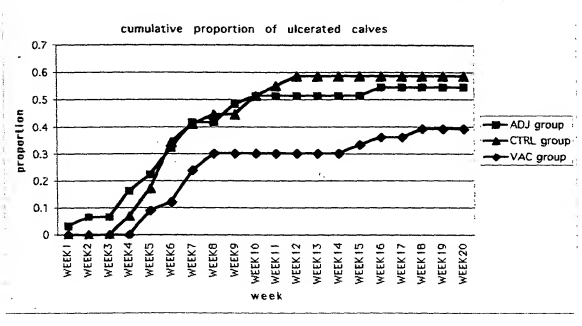


Figure 15
Number of calves affected weekly in 1 group of vaccinated calves and in controls.

FIG. 16



Cumulative proportion of ulcerated calves during the trial. Calves received as vaccines either saline (designated 'CTRL'), adjuvant alone (designated 'ADJ'), or the recombinant cytotoxin vaccine (designated 'VAC').